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## Amino acid alignment

- 1 *M. incognita* MDH1
- 2 *M. incognita* MDH2
- 3 *C. elegans* MDH1
- 4 *C. elegans* MDH2

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      .10      .20      .30      .40      .50      .60
1 .....MNY.....KDAPEFVVS PKDAREFVVK: 23
2 .....MNY.....KDAPEFVVS PKDAREFVVK: 23
3 .....MTIKDKREINETDEIVISKEKLDSEVLE: 28
4 MELLQRALVFTGGHISRYQAVIAVNSVGKNARFYSTTDDNMAAPEESVVAKDEM KREME: 60

      .70      .80      .90      .100     .110     .120
1 CMQTVGTSPDHAAGQLADLLLDADLVGHYSHGLRLRLHIYVD DVKNG.VKGNNGVEKVLKQKG: 82
2 CMQTVGTSPDHAAGQLADLLLDADLVGHYSHGLRLRLHIYVD DVKNG.VKGNNGVEKVLKQKG: 82
3 CLAKAGCTGDHAAGQLADLLLDADLVGHYSHGLRLRLHIYVD DVKNG.VKGNNGVEKVLKQKG: 88
4 CMTKVGATESHATQLALVLEGDIRGHYSHGLRLRLDMYVRDIEQNVCKGDGEPILKRENA:120

      .130     .140     .150     .160     .170     .180
1 GTARVDGEMLLGAVVGNEFC TDLAIKLAKKEFGVAWVUTENSNIYGACQHYTKKIANAGMVG:142
2 GTARVDGEMLLGAVVGNEFC TDLAIKLAKKEFGVAWVUTENSNIYGACQHYTKKIANAGMVG:142
3 STARVDGEMLLGAVVGNEFC TDLAIKLAKKEFGVAWVUTENSNIYGACQHYTKKIANAGMVG:148
4 GTARVDGEMLLGAVVGNEFC TDLAIKLAKKEFGVAWVUTENSNIYGACQHYTKKIANAGMVG:180

      .190     .200     .210     .220     .230     .240
1 MSFTTTSPLMFPCRSSEIGLGTPLSCCVNSEKTGDSFLDMATTTVALGKVELADCRGK:202
2 MSFTTTSPLMFPCRSSEIGLGTPLSCCVNSEKTGDSFLDMATTTVALGKVELADCRGK:202
3 MSFTTTSPLMFPCRSSEIGLGTPLSCCVNSEKTGDSFLDMATTTVALGKVELADCRGK:207
4 MSFTTTSPLMFPCRSSEIGLGTPLSCCVNSEKTGDSFLDMATTTVALGKVELADCRGK:238

      .250     .260     .270     .280     .290     .300
1 TQIPSTWGADSKGNPSTDTQVVLHGGGLLPLGGIEETGSGYKGTGLSMMGELFCGILAGSS:262
2 TQIPSTWGADSKGNPSTDTQVVLHGGGLLPLGGIEETGSGYKGTGLSMMGELFCGILAGSS:262
3 TQIPSTWGADSKGNPSTDTQVVLHGGGLLPLGGIEETGSGYKGTGLSMMGELFCGILAGSS:267
4 NPVPLSNGVGEKGKETDTPKVLHGGGLLPLGGIEETGSGYKGTGLSMMGELFCGILAGSS:298

      .310     .320     .330     .340     .350     .360
1 FGNIVRLWGQSHKAADNGQCFVAIDQECFAPGFAPRLQQLDETRELKPISEEEKPVILVPG:322
2 FGNIVRLWGQSHKAADNGQCFVAIDQECFAPGFAPRLQQLDETRELKPISEEEKPVILVPG:322
3 FGNIVRLWGQSHKAADNGQCFVAIDQECFAPGFAPRLQQLDETRELKPISEEEKPVILVPG:327
4 WCPHVRKRMSTKSEADNGQCFVAIDQECFAPGFAPRLQQLDETRELKPISEEEKPVILVPG:358

      .370     .380     .390     .400
1 DEERMNTEYSQKAGGLVYQEGQIKAFEEELATKCDVQMFSYKRLK.:366
2 DEERMNTEYSQKAGGLVYQEGQIKAFEEELATKCDVQMFSYKRLK.:366
3 DEERAHNMCDLGGIVYKKKQLDHEKFNADRLGVIMRLVDEKPP:372
4 DMERRHEALVEQLGGIPYHKNQITFVNDLAAKLGKTVDLVQ...:400

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FIG. 3